



1600

RAW SEQUENCE LISTING

DATE: 01/29/2003

PATENT APPLICATION: US/09/581,252

TIME: 08:10:01

Input Set : A:\2931-105.txt

Output Set: N:\CRF4\01292003\I581252.raw

3 <110> APPLICANT: Munroe, Donald
 4 Gupta, Ashwani
 5 Vyas, Tejal
 6 Chun, Jerold
 8 <120> TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS
 10 <130> FILE REFERENCE: 2931-105 (new); P108074-00003 (old)
 12 <140> CURRENT APPLICATION NUMBER: US 09/581252
 13 <141> CURRENT FILING DATE: 2000-12-04
 15 <150> PRIOR APPLICATION NUMBER: PCT/CA 98/01193
 16 <151> PRIOR FILING DATE: 1998-12-24
 18 <150> PRIOR APPLICATION NUMBER: US 08/997803
 19 <151> PRIOR FILING DATE: 1997-12-24
 21 <160> NUMBER OF SEQ ID NOS: 29
 23 <170> SOFTWARE: PatentIn version 3.2
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 32
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Degenerate PCR primer: A1
 34 <220> FEATURE:
 35 <221> NAME/KEY: misc_feature
 36 <222> LOCATION: (1)..(32)
 37 <223> OTHER INFORMATION: n = i
 39 <400> SEQUENCE: 1

ENTERED
 P.6

W--> 40 aaytrsatnm tnstnaayyt ngcngtngcn ga

32

43 <210> SEQ ID NO: 2
 44 <211> LENGTH: 33
 45 <212> TYPE: DNA
 46 <213> ORGANISM: Artificial Sequence
 48 <220> FEATURE:
 49 <223> OTHER INFORMATION: Degenerate PCR primer: B1
 52 <220> FEATURE:
 53 <221> NAME/KEY: misc_feature
 54 <222> LOCATION: (1)..(33)
 55 <223> OTHER INFORMATION: n = i
 57 <400> SEQUENCE: 2

W--> 58 ctgnykwttc atnawnmmrt anaynayngg rtt

33

61 <210> SEQ ID NO: 3
 62 <211> LENGTH: 639
 63 <212> TYPE: DNA
 64 <213> ORGANISM: Artificial Sequence
 66 <220> FEATURE:

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71 <221> NAME/KEY: misc_feature
72 <222> LOCATION: (126)..(628)
73 <223> OTHER INFORMATION: n = unknown
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78 ctagacacca gcctgactgc ctccctggcc aatttgctgg ttattgctgt ggaaagacac      120
W--> 80 atgtcnatca tgaggatgag agtccacagc aacttgacca aaaagcgggt gacgctgctc      180
W--> 82 attctgctgg tgtggggccat cgccatcttc atggggggccg tccccacnct gggatggaat      240
84 tgcctctgca acatctcggc ctgctcttct ctggctccca ttacagtag gagttacctc      300
86 attttctgga ctgtgtccaa cctcctggcc ttcttcatca tgggtggcgt atacgtacgc      360
88 atctacatgt atgttaaaag gaaaaccaac gtcttatctc cacacaccag tggctccatc      420
90 agccgccgga gggctcccat gaagctaata aagacagtga tgaccgtctt aggcgccttc      480
92 gtgggtgtgct ggaccccggt tctggtggtt ctgctgctgg acggcctgaa ctgcaagcag      540
W--> 94 tgtaacgtgc aacacgtgaa gngctggttc ctgctgctcg cactgctcaa ctccgtcatg      600
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101 <212> TYPE: DNA
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105 <223> OTHER INFORMATION: PCR primer: JC501-F2
107 <400> SEQUENCE: 4
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112 <211> LENGTH: 37
113 <212> TYPE: DNA
114 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: PCR primer: JC501-R
119 <400> SEQUENCE: 5
120 ttttttctag acggtcatca ctgtcttcat tagcttc      37
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124 <211> LENGTH: 30
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
128 <220> FEATURE:
129 <223> OTHER INFORMATION: PCR primer: H501-20F
131 <400> SEQUENCE: 6
132 atgcggctgc atagcaacct gacaaaaaag      30
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136 <211> LENGTH: 30
137 <212> TYPE: DNA
138 <213> ORGANISM: Artificial Sequence
140 <220> FEATURE:
141 <223> OTHER INFORMATION: PCR primer: H501-246R
143 <400> SEQUENCE: 7
144 atccgcaggt acaccacaac catgatgagg      30

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147 <210> SEQ ID NO: 8
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149 <212> TYPE: DNA
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153 <223> OTHER INFORMATION: PCR primer: GT10-F
155 <400> SEQUENCE: 8
156 ttttgagcaa gttcagcctg gttaagt 27
159 <210> SEQ ID NO: 9
160 <211> LENGTH: 27
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: PCR primer: GT10-R
167 <400> SEQUENCE: 9
168 tggcttatga gtatttcttc cagggtta 27
171 <210> SEQ ID NO: 10
172 <211> LENGTH: 32
173 <212> TYPE: DNA
174 <213> ORGANISM: Artificial Sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: PCR primer: GT10-5KX-b
179 <400> SEQUENCE: 10
180 gggtagtcgg tacctctaga gcaagttcag cc 32
183 <210> SEQ ID NO: 11
184 <211> LENGTH: 31
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: PCR primer: GT10-3BXh
191 <400> SEQUENCE: 11
192 ataacagagg atcctcgagt atttcttcca g 31
195 <210> SEQ ID NO: 12
196 <211> LENGTH: 1523
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
200 <220> FEATURE:
201 <223> OTHER INFORMATION: Nucleotide sequence of the genomic DNA flanking 5' end of
the
202 hedg-5 cDNA insert of pC3-hedg-55 clone and the hedg-5 cDNA
204 <400> SEQUENCE: 12
205 caccttccta acctgagcgg cctagcctgg gaaacaaaca attaaaatgt gcgctaaatg 60
207 ctgtggtagg aggtcagggg ctatgtcctg gaccaaagga catttgact gagacctgac 120
209 acttcaggtc ttcaactccc ttgatgggag ttagccagaa cgggcttaga aacagcaatt 180
211 gatggcttag tgactgattt tacaaatgat atttgtttct tctttaaatt tctttctagg 240
213 atgttcactt cttctccaca atgaatgagt gtcactatga caagcacatg gacttttttt 300
215 ataataggag caacactgat actgtcgatg actggacagg aacaaagctt gtgattgttt 360
217 tgtgtgttgg gacgtttttc tgectgttta tttttttttc taattctctg gtcacgcgag 420
219 cagtgatcaa aaacagaaaa tttcattttcc ccttttacta cctgttggtt aatttagctg 480
221 ctgccgattt cttcgctgga attgcctatg tattcctgat gtttaacaca ggcccagttt 540

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223 caaaaacttt gactgtcaac cgctgggttc tccgtcaggg gcttctggac agtagcttga 600
225 ctgcttccct caccaacttg ctggttatcg ccgtggagag gcacatgtca atcatgagga 660
227 tgcgggtcca tagcaacctg accaaaaaga gggtgacact gtcatttttg cttgtctggg 720
229 ccatcgccat ttttatgggg gcggtcccca cactgggctg gaattgcctc tgcaacatct 780
231 ctgcctgctc ttccctggcc cccatttaca gcaggagtta ccttgttttc tggacagtgt 840
233 ccaacctcat ggccttccct atcatggttg tgggtgtacct gcggatctac gtgtacgtca 900
235 agaggaaaac caacgtcttg tctccgcata caagtgggtc catcagccgc cggaggacac 960
237 ccatgaagct aatgaagacg gtgatgactg tcttaggggc gtttgtggta tgcctggacc 1020
239 cgggctgggt ggttctgccc ctgcacggcc tgaactgcag gcagtgtggc gtgcagcatg 1080
241 tgaaaaggtg gttcctgctg ctggcgctgc tcaactccgt cgtgaacccc atcatctact 1140
243 cctacaagga cgaggacatg tatggcacca tgaagaagat gatctgctgc ttctctcagg 1200
245 agaaccaga gaggcgtccc tctcgcatcc cctccacagt cctcagcagg agtgacacag 1260
247 gcagccagta catagaggat agtattagcc aagggtcagt ctgcaataaa agcacttcct 1320
249 aaactctgga tgcctctygg cccaccagg cctcctctgg gaaaagagct gttaagaatg 1380
251 attacctgtc tctaacaaag cccatgtaca gtgttatttg aggtctccat taatcactgc 1440
253 tagatttctt taaaaaattt tttttcatag tttaaaagca tgggcagtaa agagaggacc 1500
255 tgctgcattt agagaaagca cag 1523
258 <210> SEQ ID NO: 13
259 <211> LENGTH: 1357
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Nucleotide sequence of a hEDG-5 cDNA inserted into pcDNA3
266 <400> SEQUENCE: 13
267 gaattcgcg cgcgctcgac gttcacttct ccacaatgaa tgagtgtcac tatgacaagc 60
269 acatggactt tttttataat aggagcaaca ctgatactgt cgatgactgg acaggaacaa 120
271 agcttgtgat tgttttgtgt gttgggacgt ttttctgcct gtttattttt ttttctaatt 180
273 ctctggtcat cgcggcagtg atcaaaaaca gaaaatttca tttccctttt tactacctgt 240
275 tggctaattt agctgctgcc gatttcttcg ctggaattgc ctatgtattc ctgatgttta 300
277 acacaggccc agtttcaaaa actttgactg tcaaccgctg gtttctccgt caggggcttc 360
279 tggacagtag cttgactgct tccctcacca acttgctggg tategccgtg gagaggcaca 420
281 tgtcaatcat gaggatgcgg gtccatagca acctgaccaa aaagagggtg aactgtctca 480
283 ttttgcttgt ctgggccatc gccattttta tgggggcggt cccacactg ggctggaatt 540
285 gcctctgcaa catctctgcc tgccttccc tggcccccac ttacagcagg agttaccttg 600
287 ttttctggac agtgtccaac ctcatggcct tcctcatcat ggttgtgggt tacctgcgga 660
289 tctacgtgta cgtcaagagg aaaaccaacg tcttgtctcc gcatacaagt ggggccatca 720
291 gccgccggag gacacccatg aagctaataa agacggtgat gactgtctta ggggcgtttg 780
293 tggatagctg gaccccgggc ctggtggttc tgcccctcga cggcctgaac tgcaggcagt 840
295 gtggcgtgca gcatgtgaaa aggtggttcc tgctgctggc gctgctcaac tccgtcgtga 900
297 accccatcat ctactcctac aaggacgagg acatgtatgg caccatgaag aagatgatct 960
299 gctgcttctc tcaggagaac ccagagaggc gtccctctcg catcccctcc acagtctca 1020
301 gcaggagtga cacaggcagc cagtacatag aggatagtat tagccaaggt gcagtctgca 1080
303 ataaaagcac ttctaaact ctggtagcct ctyggcccac ccaggcctcc tctgggaaaa 1140
305 gacgtgttaa gaatgattac ctgtctctaa caaagcccac gtacagtgtt atttgaggtc 1200
307 tccattaatc actgctagat ttctttaaaa aatttttttt catagttaa aagcatgggc 1260
309 agtaaagaga ggacctgctg catttagaga aagcacaggt cgacgcggcc gcgaattctt 1320
311 ttgcttttta cctggaaga aatactcgag catgcat 1357
314 <210> SEQ ID NO: 14
315 <211> LENGTH: 353

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316 <212> TYPE: PRT
317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
320 <223> OTHER INFORMATION: Predicited amino acid sequence of pC3-hedg-55 clone
322 <400> SEQUENCE: 14
324 Met Asn Glu Cys His Tyr Asp Lys His Met Asp Phe Phe Tyr Asn Arg
325 1 5 10 15
328 Ser Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile
329 20 25 30
332 Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn
333 35 40 45
336 Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro
337 50 55 60
340 Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Ala Asp Phe Phe Ala Gly
341 65 70 75 80
344 Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr
345 85 90 95
348 Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser
349 100 105 110
352 Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His
353 115 120 125
356 Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg
357 130 135 140
360 Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly
361 145 150 155 160
364 Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys
365 165 170 175
368 Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr
369 180 185 190
372 Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg
373 195 200 205
376 Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr
377 210 215 220
380 Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr
381 225 230 235 240
384 Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu
385 245 250 255
388 Val Val Leu Pro Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln
389 260 265 270
392 His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val
393 275 280 285
396 Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met
397 290 295 300
400 Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro
401 305 310 315 320
404 Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln
405 325 330 335
408 Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr
409 340 345 350

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 9,12,15,21,24,27,30
Seq#:2; N Pos. 4,13,16,22,25,28
Seq#:3; N Pos. 126,228,562,627,628
Seq#:15; Xaa Pos. 188,210